

FIG. 2 (a) pYE22m / PINORESINOL

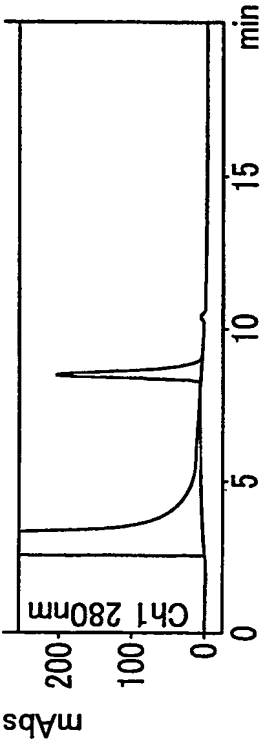


FIG. 2 (d) pYE22m / PIPERITOL

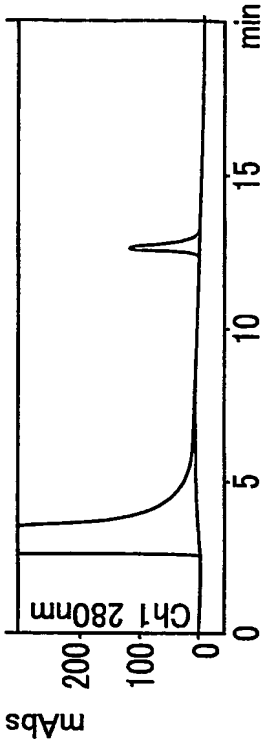


FIG. 2 (b) SiP189 / PINORESINOL

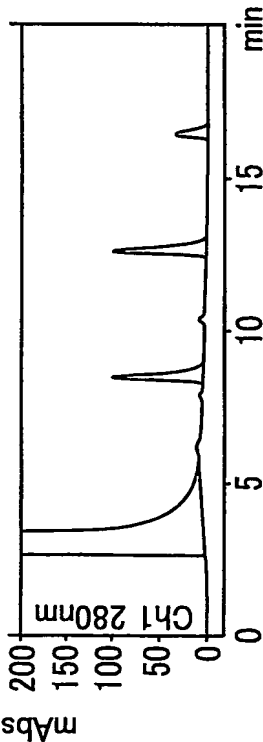


FIG. 2 (e) SiP189 / PIPERITOL

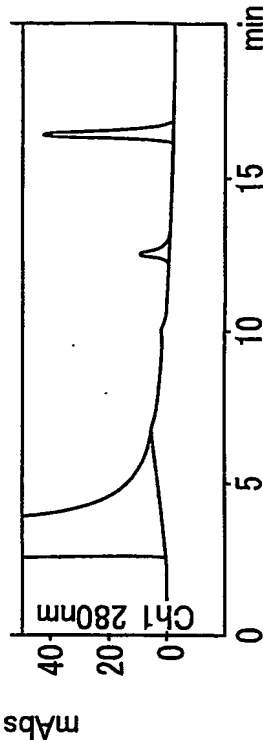


FIG. 2 (c) SiP189 / PINORESINOL

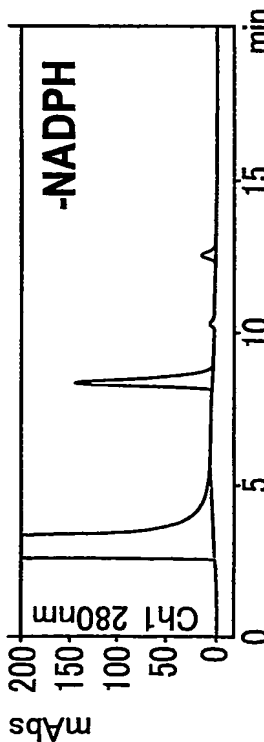
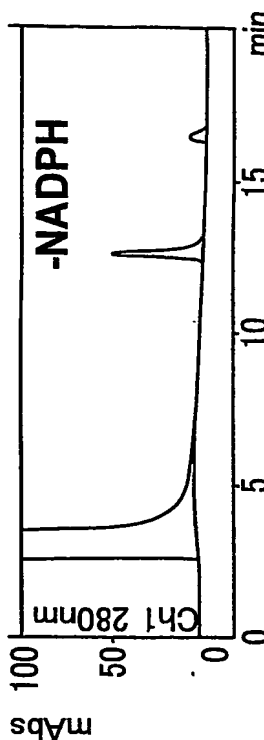
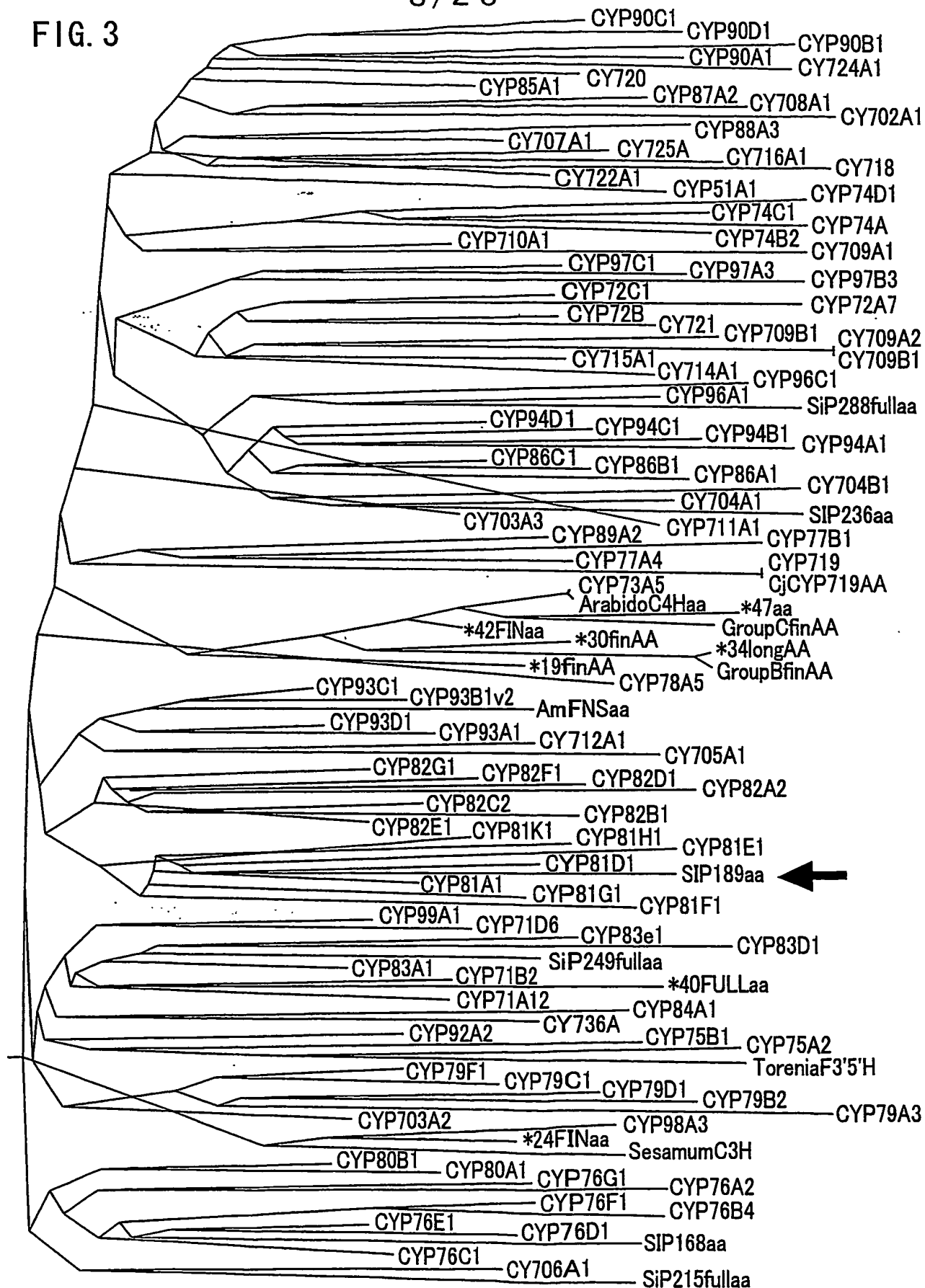


FIG. 2 (f) SiP189 / PIPERITOL



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FIG. 3



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FIG. 4

> Blastx Search (SST vs PIR)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= BXP184.2003.08.12
(1521 letters)

Database: pir1.fst; pir2.fst; pir3.fst; pir4.fst
283,329 sequences; 96,175,589 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<u>T04730</u> (PIR) cytochrome P450 homolog F6G17.10 - Arabidopsis thal...	<u>494</u>	e-139
<u>C85441</u> (PIR) cytochrome P450-like protein [imported] - Arabidopsis	<u>494</u>	e-139
<u>T52174</u> (PIR) cytochrome P450 monooxygenase [imported] - Arabidopsis	<u>487</u>	e-137
<u>B85441</u> (PIR) cytochrome P450-like protein [imported] - Arabidopsis	<u>481</u>	e-135
<u>T04731</u> (PIR) cytochrome P450 homolog F6G17.20 - Arabidopsis thal...	<u>480</u>	e-135
<u>T10896</u> (PIR) cytochrome P450 (EC 1.14.-.-) 81B1c - Jerusalem art...	<u>468</u>	e-131
<u>A85441</u> (PIR) cytochrome P450-like protein [imported] - Arabidopsis	<u>464</u>	e-130
<u>T00510</u> (PIR) probable cytochrome P450 At2g23220 [imported] - Ara...	<u>457</u>	e-128
<u>T00513</u> (PIR) cytochrome P450 homolog At2g23190 - Arabidopsis tha...	<u>453</u>	e-127
<u>B96691</u> (PIR) probable cytochrome P450 F28G11.4 [imported] - Arab...	<u>444</u>	e-124

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FIG. 5

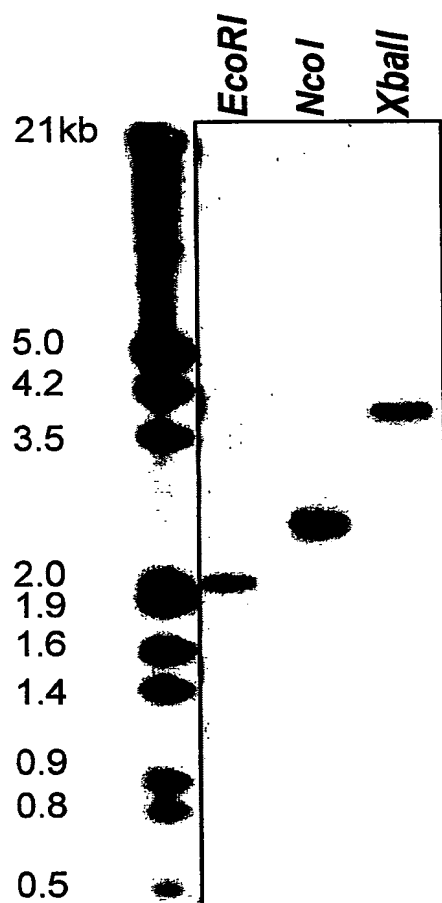


FIG. 6 (a) **SrSiP189/ PINORESINOL**

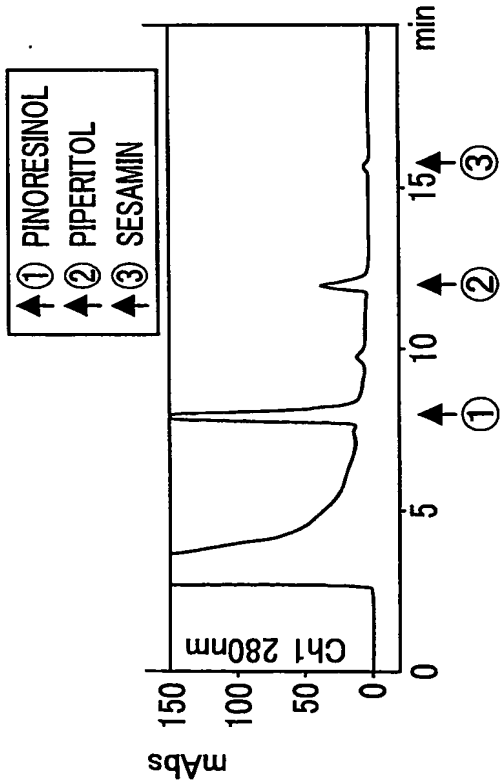


FIG. 6 (b) **SrSiP189/ PIPERITOL**

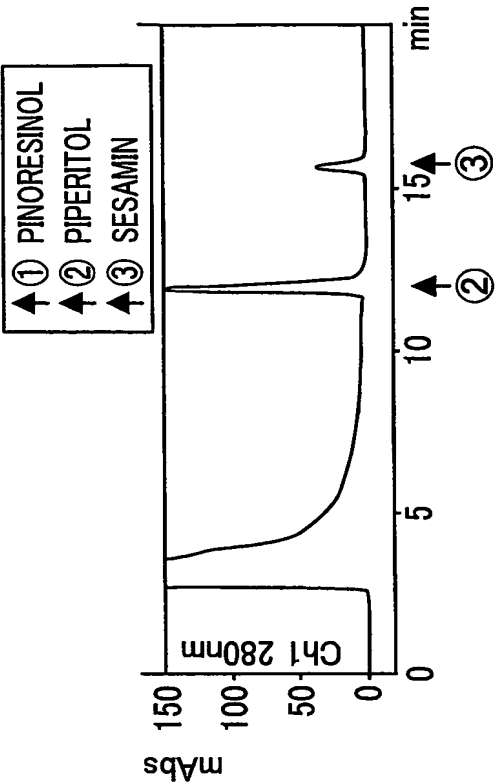


FIG. 6 (c) **SrSiP189/ PINORESINOL**

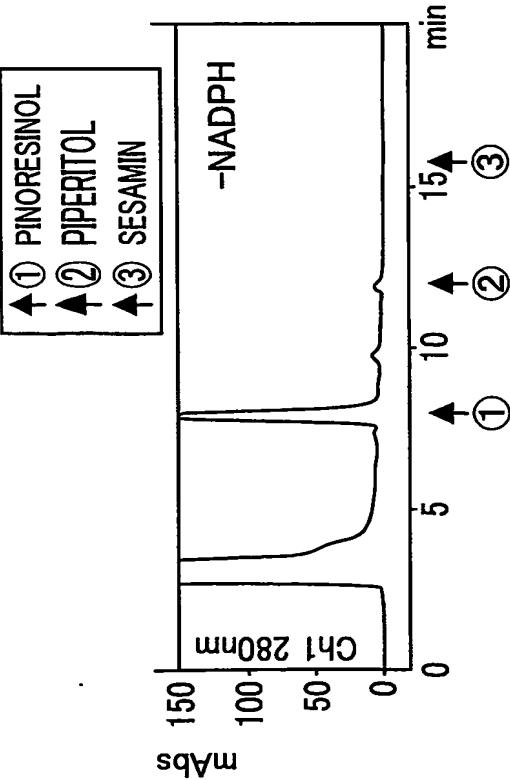
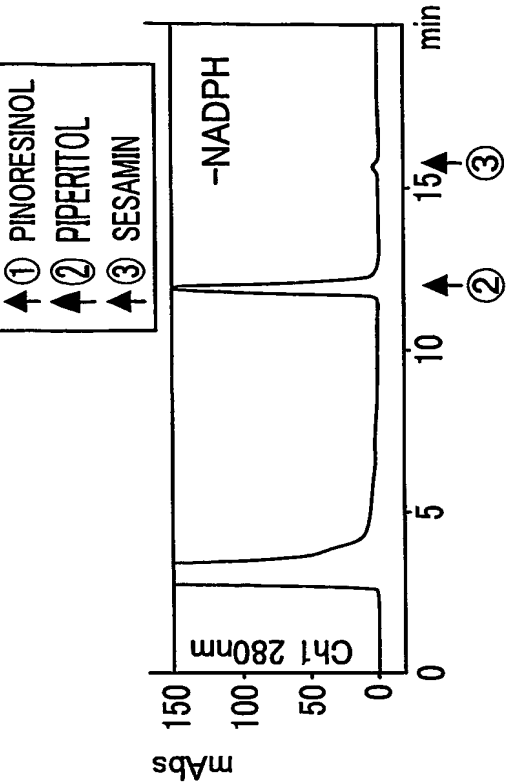


FIG. 6 (d) **SrSiP189/ PIPERITOL**



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FIG. 7

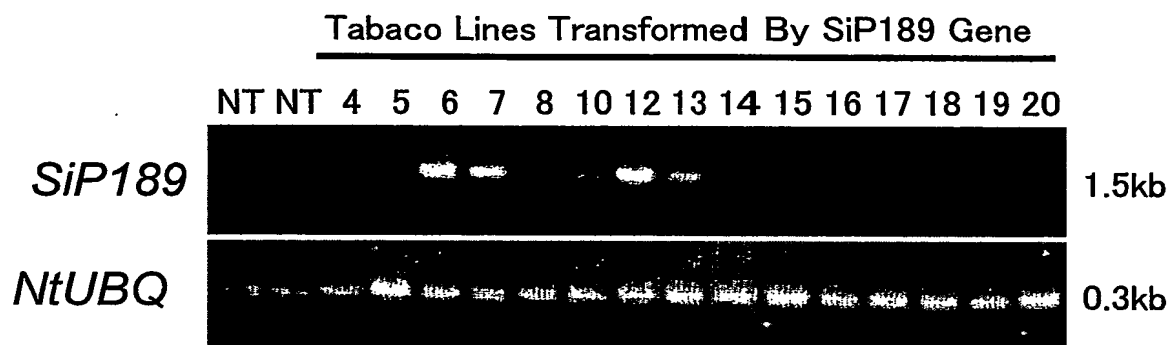


FIG. 8(a)

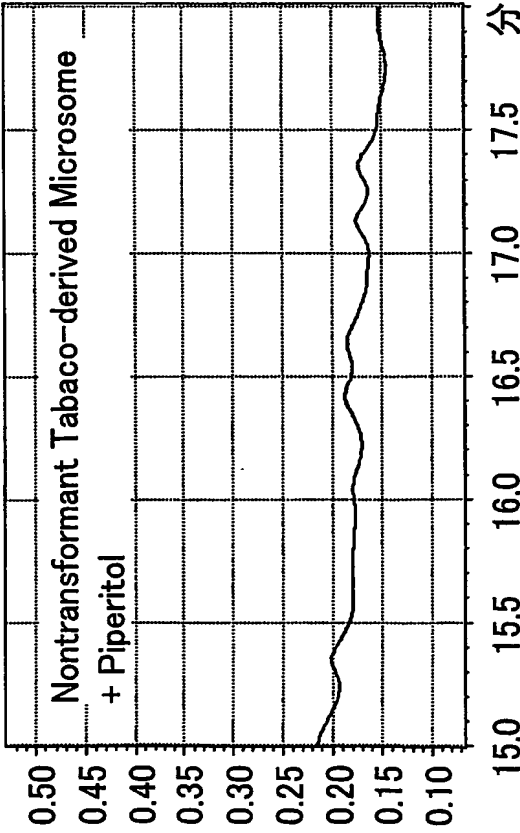


FIG. 8(b)

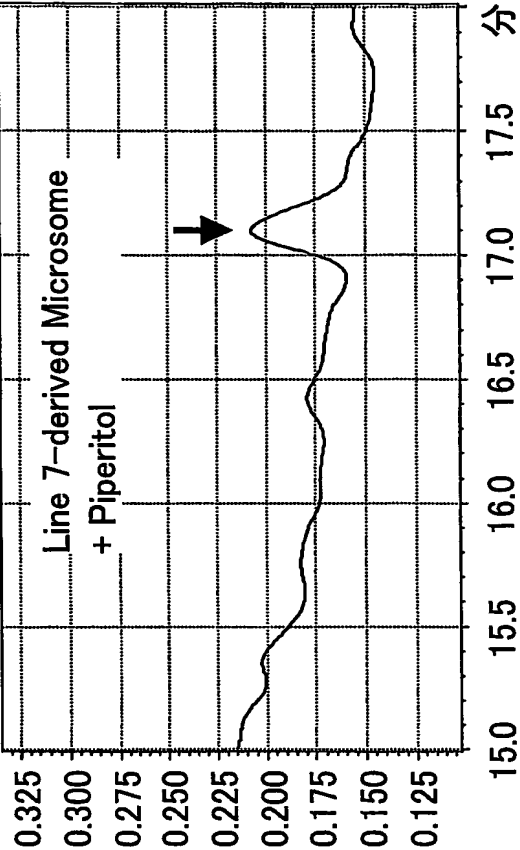


FIG. 8(c)

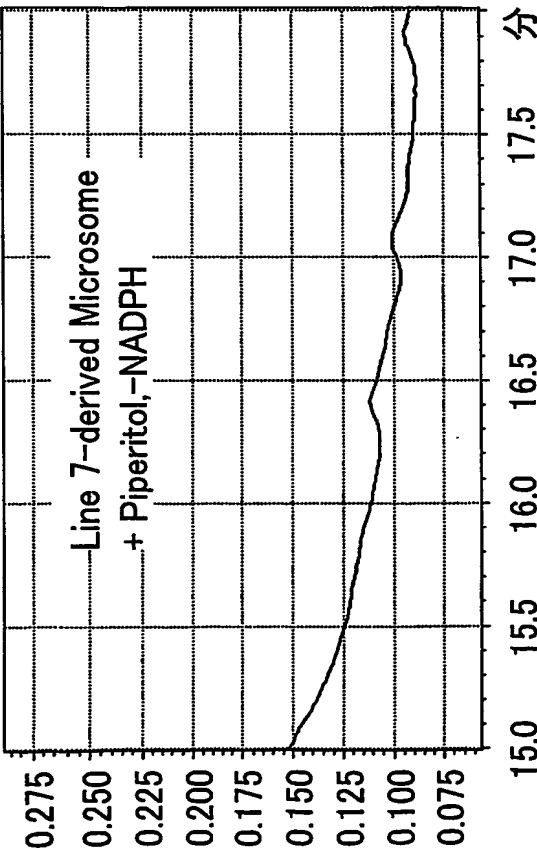


FIG. 8(d)

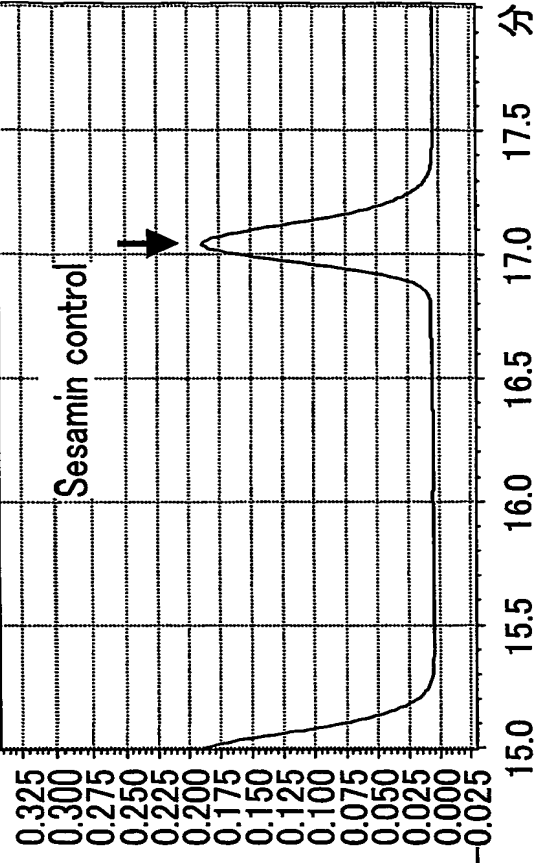
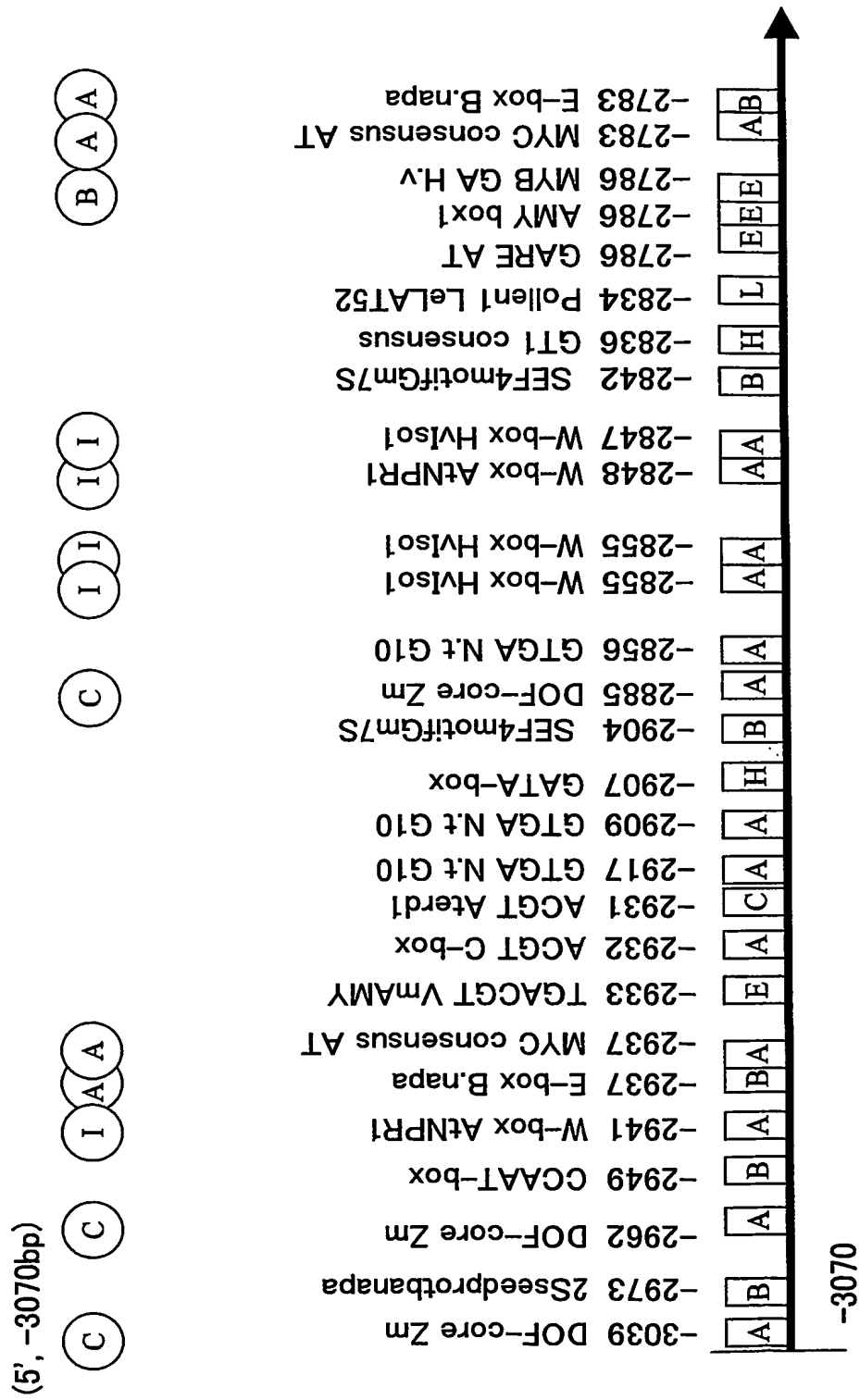
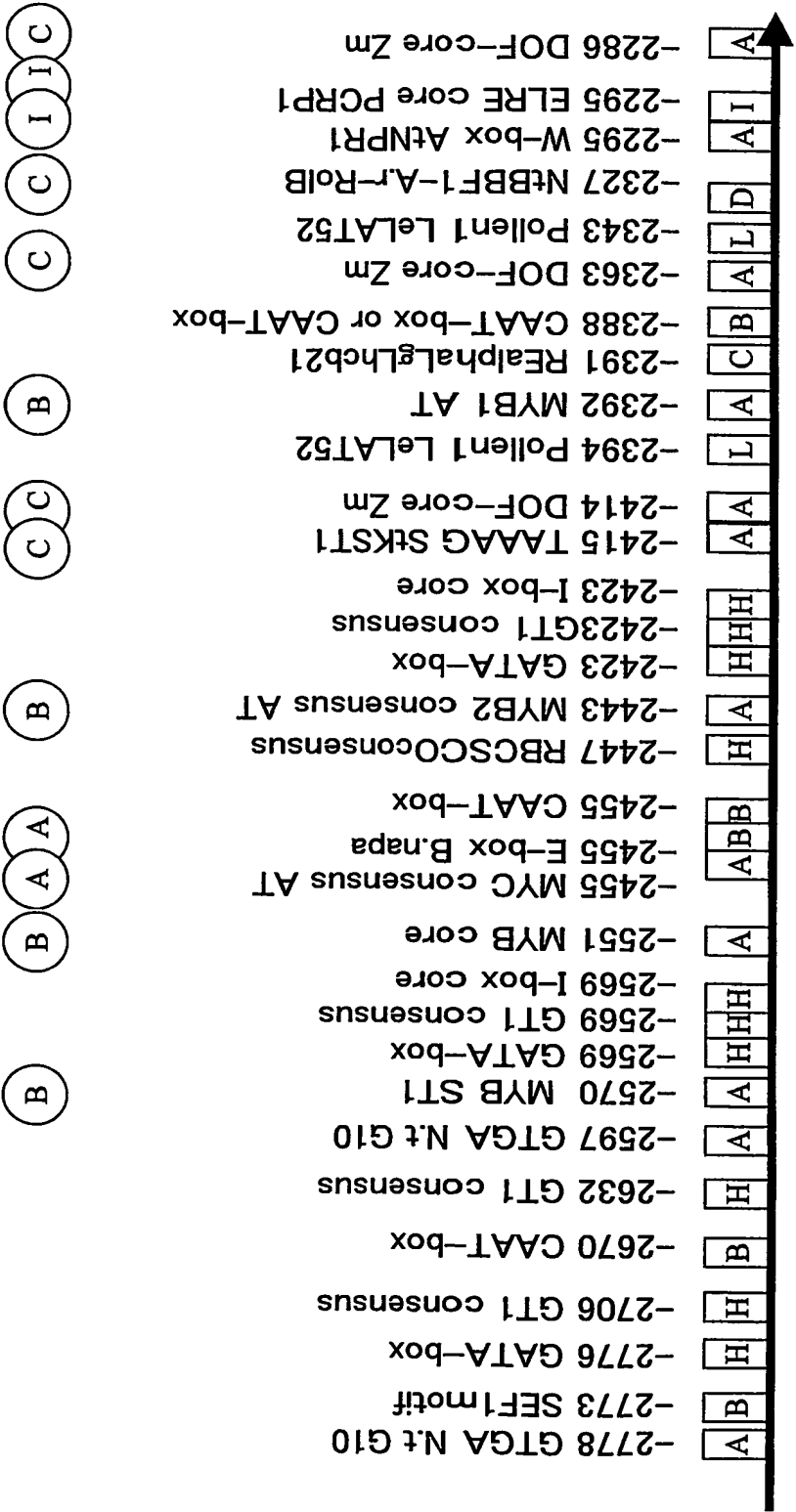


FIG. 9(A)



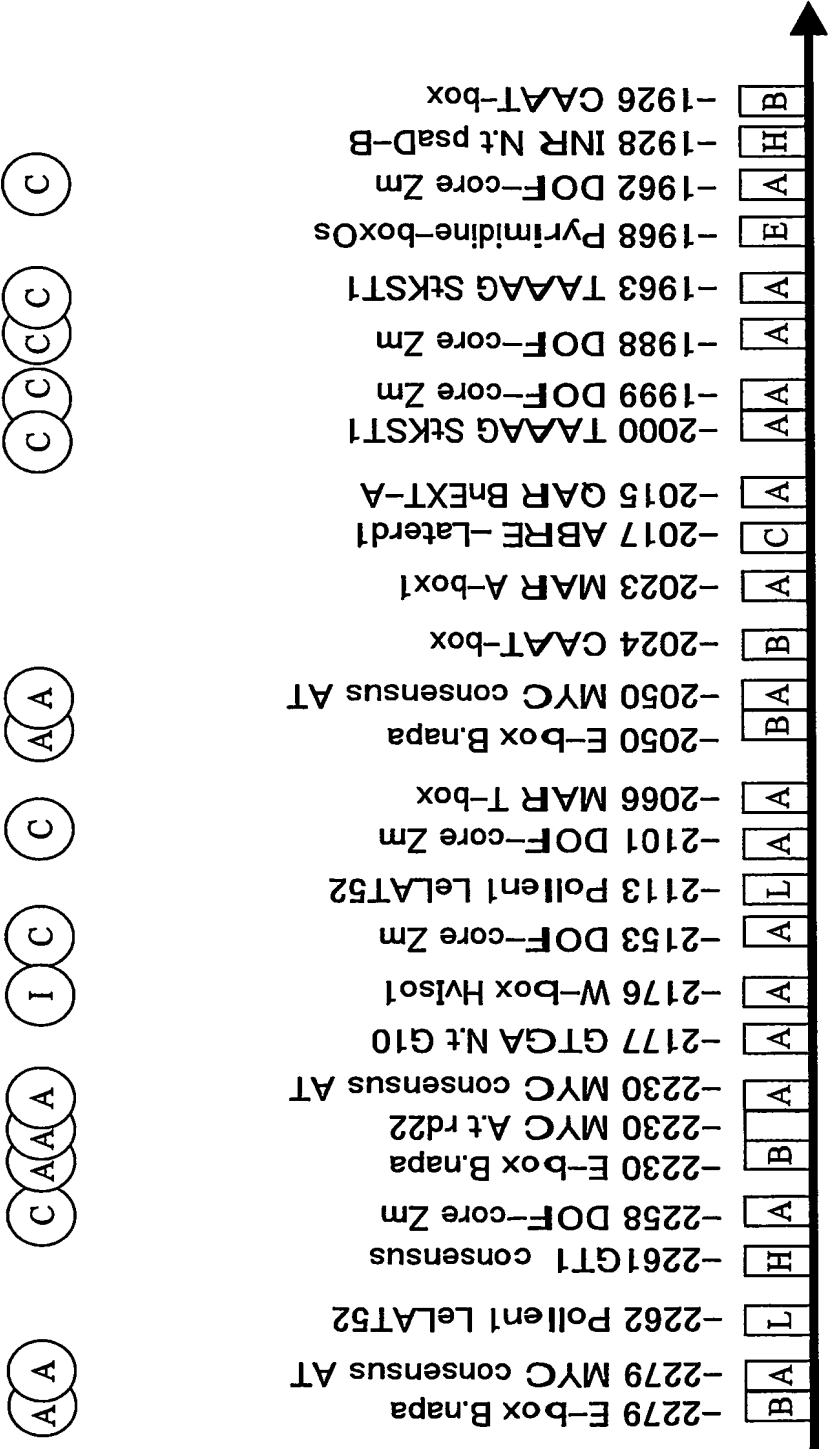
9 2 / 0 1

FIG. 9(B)



9 1 / 1 2 6

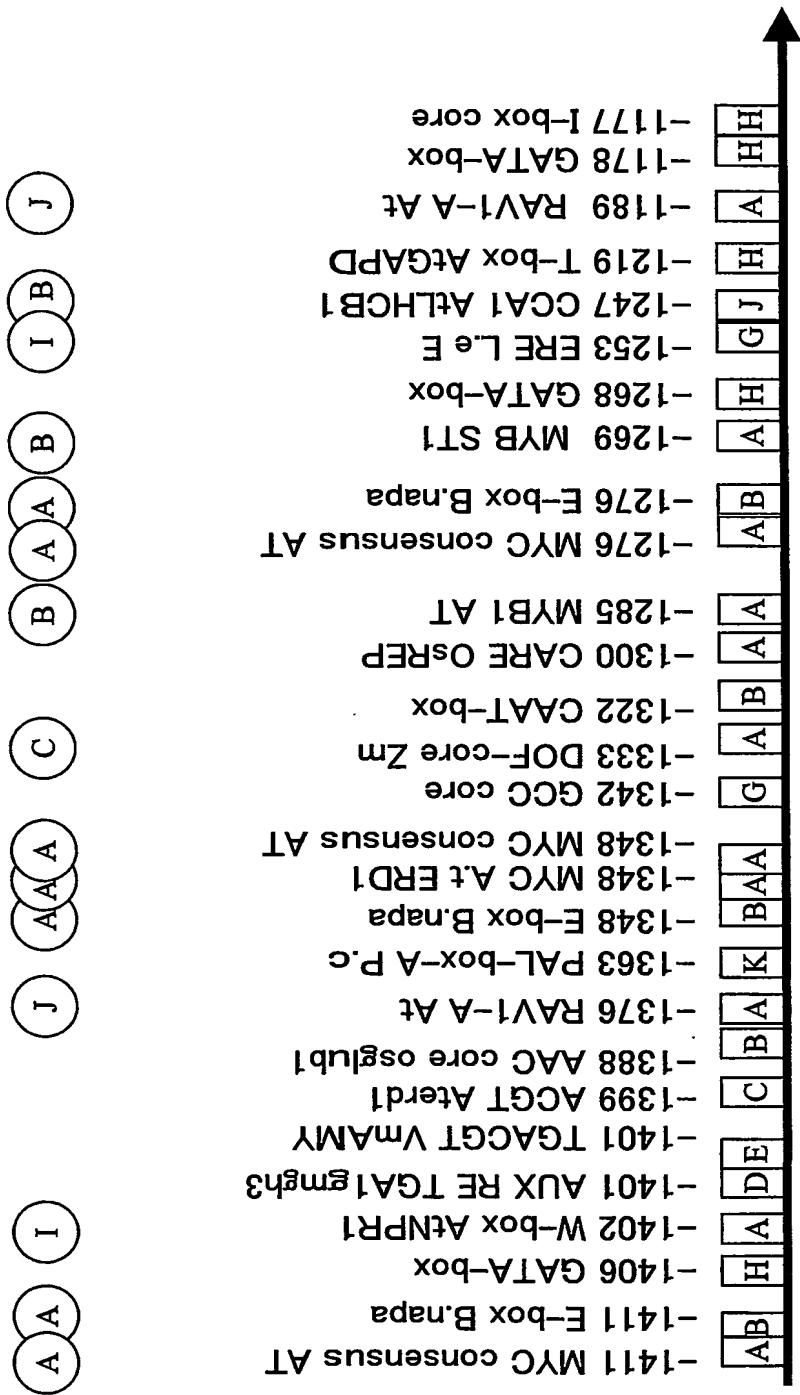
FIG. 9(G)



Accession	Gene	Species	Chromosome	Start (kb)	End (kb)	Orientation	Feature
-1908	GTGA N.t G10	Nicotiana glauca	1	1000000	1000100	+	5'UTR
-1905	AAC core osglub1	Nicotiana glauca	1	1000100	1000200	+	5'UTR
-1900	ACGT Aterd1	Nicotiana glauca	1	1000200	1000300	+	5'UTR
-1891	WUS AtAG	Arabidopsis thaliana	5	1000300	1000400	+	5'UTR
-1884	TATCGAC OsAMY	Oryza sativa	1	1000400	1000500	+	5'UTR
-1884	TATCGAC HVAL21	Hordeum vulgare	1	1000500	1000600	+	5'UTR
-1877	GATA-box	Arabidopsis thaliana	5	1000600	1000700	+	5'UTR
-1833	CAAT-box	Arabidopsis thaliana	5	1000700	1000800	+	5'UTR
-1800	TAAAG StKST1	Solanum tuberosum	1	1000800	1000900	+	5'UTR
-1799	DOF-core Zm	Zea mays	1	1000900	1001000	+	5'UTR
-1762	CGAAT-box	Arabidopsis thaliana	5	1001000	1001100	+	5'UTR
-1735	DOF-core Zm	Zea mays	1	1001100	1001200	+	5'UTR
-1654	MAR T-box	Arabidopsis thaliana	5	1001200	1001300	+	5'UTR
-1629	MYB core	Arabidopsis thaliana	5	1001300	1001400	+	5'UTR
-1634	ARF AT	Arabidopsis thaliana	5	1001400	1001500	+	5'UTR
-1628	CER Glu-box1 PsLegA	Phaseolus sativus	1	1001500	1001600	+	5'UTR
-1625	TAAAG StKST1	Solanum tuberosum	1	1001600	1001700	+	5'UTR
-1624	DOF-core Zm	Zea mays	1	1001700	1001800	+	5'UTR
-1597	CAR-G-box (AGL15)	Arabidopsis thaliana	5	1001800	1001900	+	5'UTR
-1587	SV40coreEnhancer	Simian virus 40	1	1001900	1002000	+	5'UTR
-1573	DOF-core Zm	Zea mays	1	1002000	1002100	+	5'UTR
-1563	E-box B.napa	Brassica napus	1	1002100	1002200	+	5'UTR
-1563	MYC consensus AT	Arabidopsis thaliana	5	1002200	1002300	+	5'UTR
-1503	MYB P Z.m	Zea mays	1	1002300	1002400	+	5'UTR
-1501	SEF3motifGm	Glycine max	1	1002400	1002500	+	5'UTR
-1486	QelementZmZM13	Zea mays	1	1002500	1002600	+	5'UTR
-1473	RAV1-A At	Arabidopsis thaliana	5	1002600	1002700	+	5'UTR
-1434	E-box B.napa	Brassica napus	1	1002700	1002800	+	5'UTR
-1434	CATATG GM SAUR	Glycine max	1	1002800	1002900	+	5'UTR
-1434	MYC consensus AT	Arabidopsis thaliana	5	1002900	1003000	+	5'UTR

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FIG. 9(E)



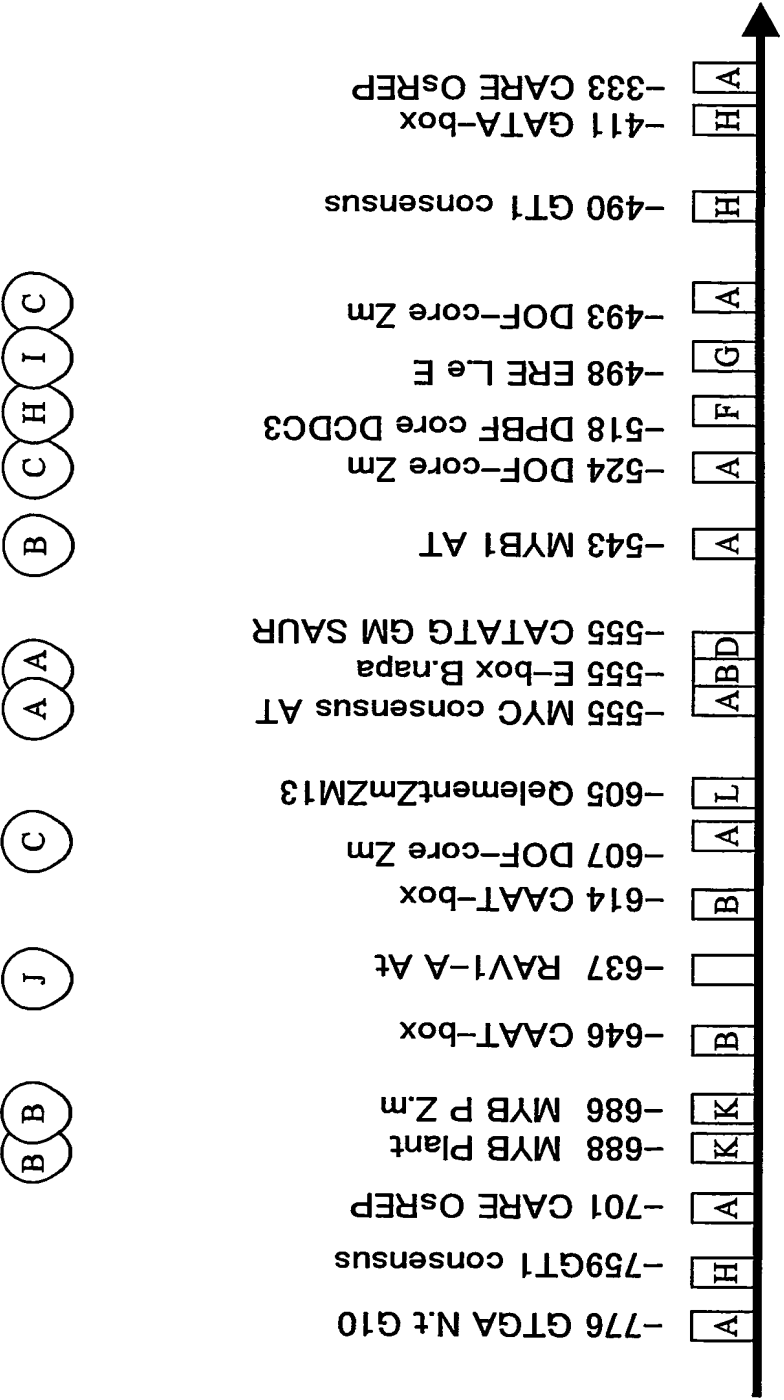
Accession	Category	Value
-1158 GTGA N.t G10	A	H
-1147 GATA-box	A	H
-1142 TATCAG O.sAMY	E	K
-1139 MYB P Z.m	K	
-1134 MYC consensus AT	A	A
-1134 MYB core	A	B
-1134 E-box B.napa	B	A
-1116 TAAAG StKST1	A	A
-1115 DOF-core Zm	A	B
-1109 CAAT-box	B	
-1091 DOF-core Zm	A	
-1087 CCAAT-box	B	A
-1098 RAV1-A At	A	B
-1086 CAAT-box	B	
-1067 CARG-box (AGL15)	B	
-1047 W-box HvIsol	A	
-1022 INR N.t psad-B	H	B
-1020 CAAT-box	H	B
-992 GATA-box	H	
-987 INR N.t psad-B	H	H
-949 CARG-box (AGL15)	B	
-914 WB-box PcWRKY1	A	A
-913 W-box AtNPR1	A	A
-912 W-box HvIsol	A	A
-902 RAV1-A At	A	B
-899 CAAT-box	B	L
-856 Pollen1 LeLAT52	L	
-853 DOF-core Zm	A	
-811 TAAAG StKST1	A	A
-810 DOF-core Zm	A	A
-791 DOF-core Zm	A	A
-779 DOF-core Zm	A	A

FIG. 9(F)



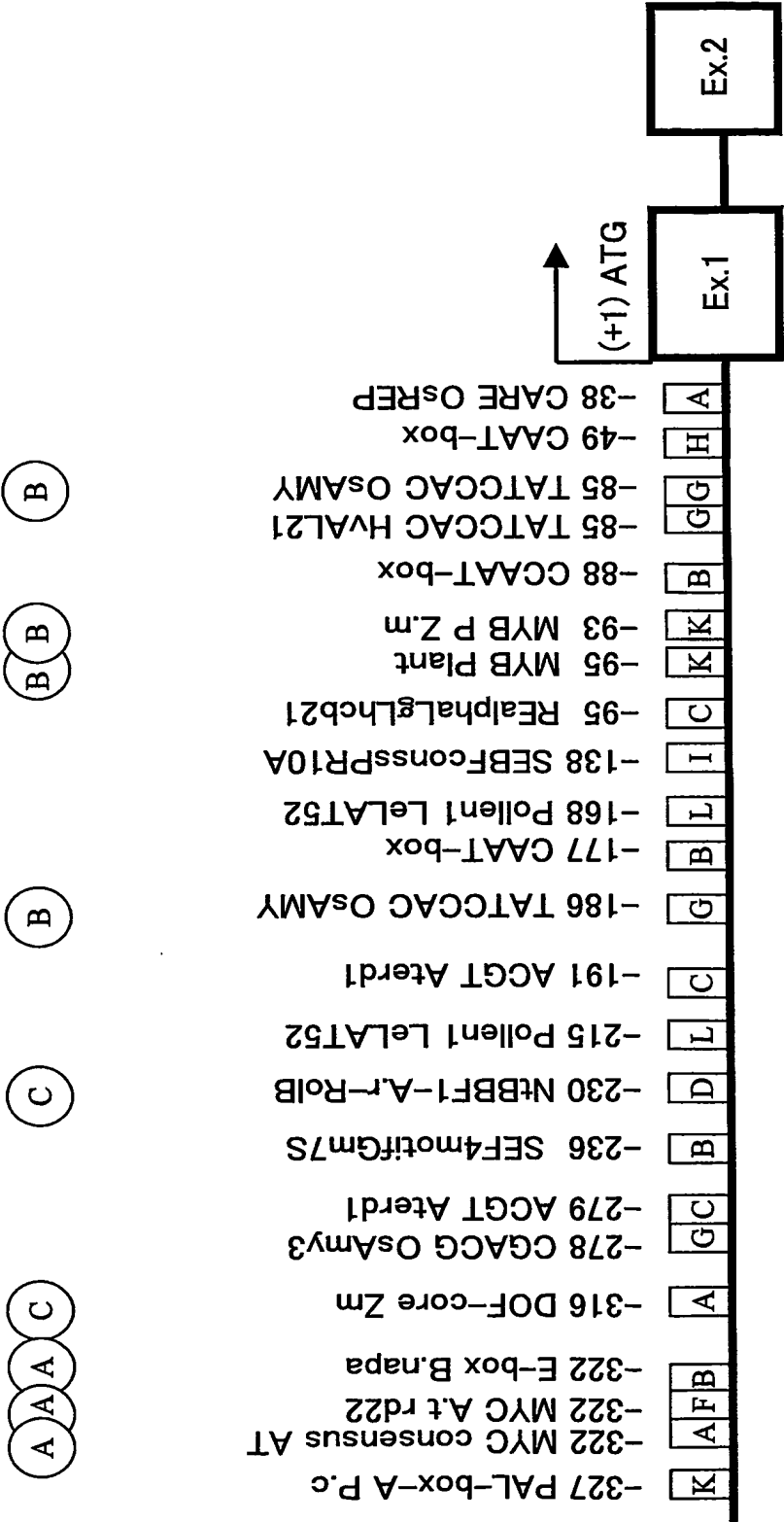
1 5 / 2 6

FIG. 9 (G)



1 6 / 2 6

FIG. 9(H)



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FIG. 10

Putative Physiological response

- A Unknown
- B Seed/endosperm/embryo-related
- C Etiolation-related
- D Auxin-related
- E GA/amylase-related
- F ABA-related
- G Ethylen-related
- H Light-regulated
- I Pathogenesis-related
- J Circadian clock-regulated
- K Secondary metabolism-related
- L Pollen development

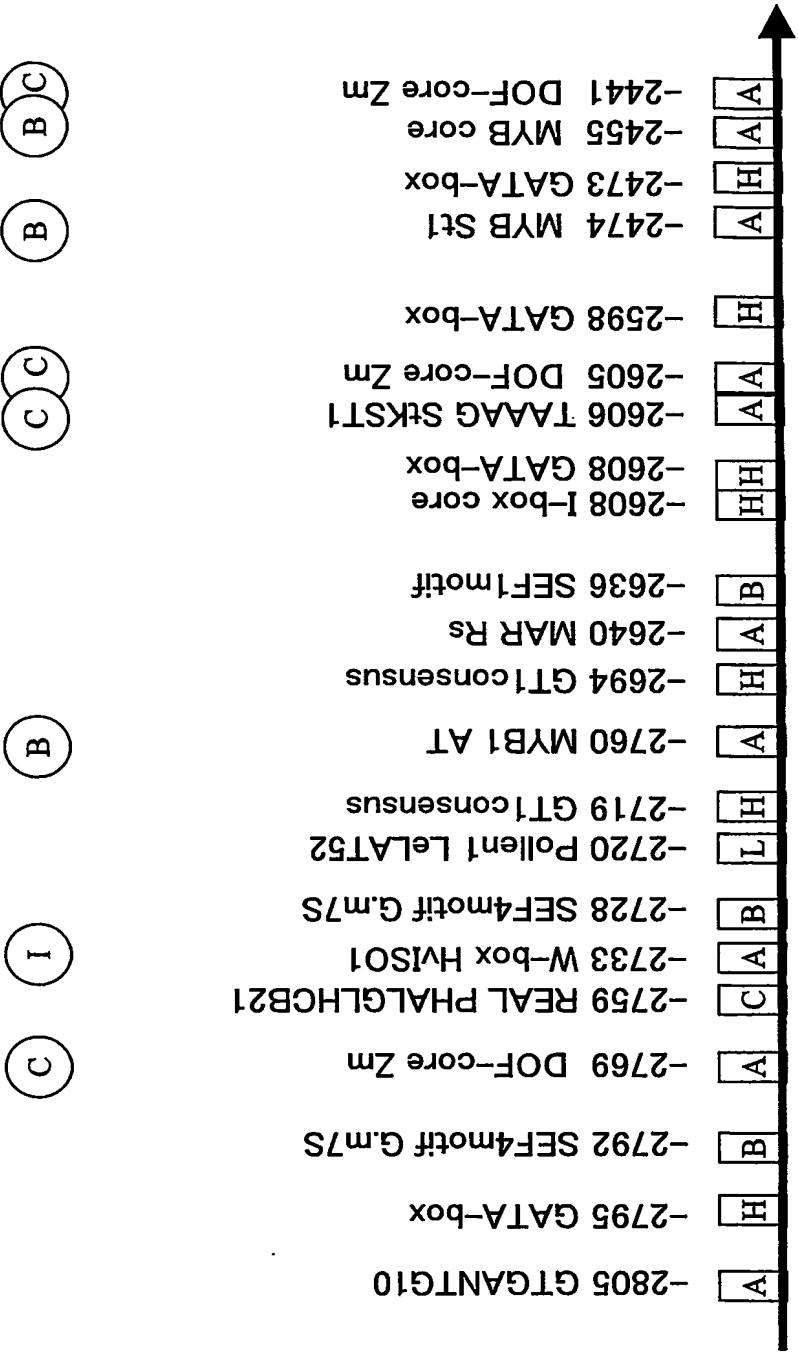
Putative structure of target *trans*-factor

- A Myc (bHLH class)
- B Myb
- C Zinc Finger (Dof class)
- D Homeobox
- E MADS
- F ARF
- G Leucine Zipper (TGA class)
- H bZIP (DPBF class)
- I WRKY
- J AP2-domain (RAV class)

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FIG. 11 (A)

2815bp



9 2 / 6 1

FIG. 11 (B)

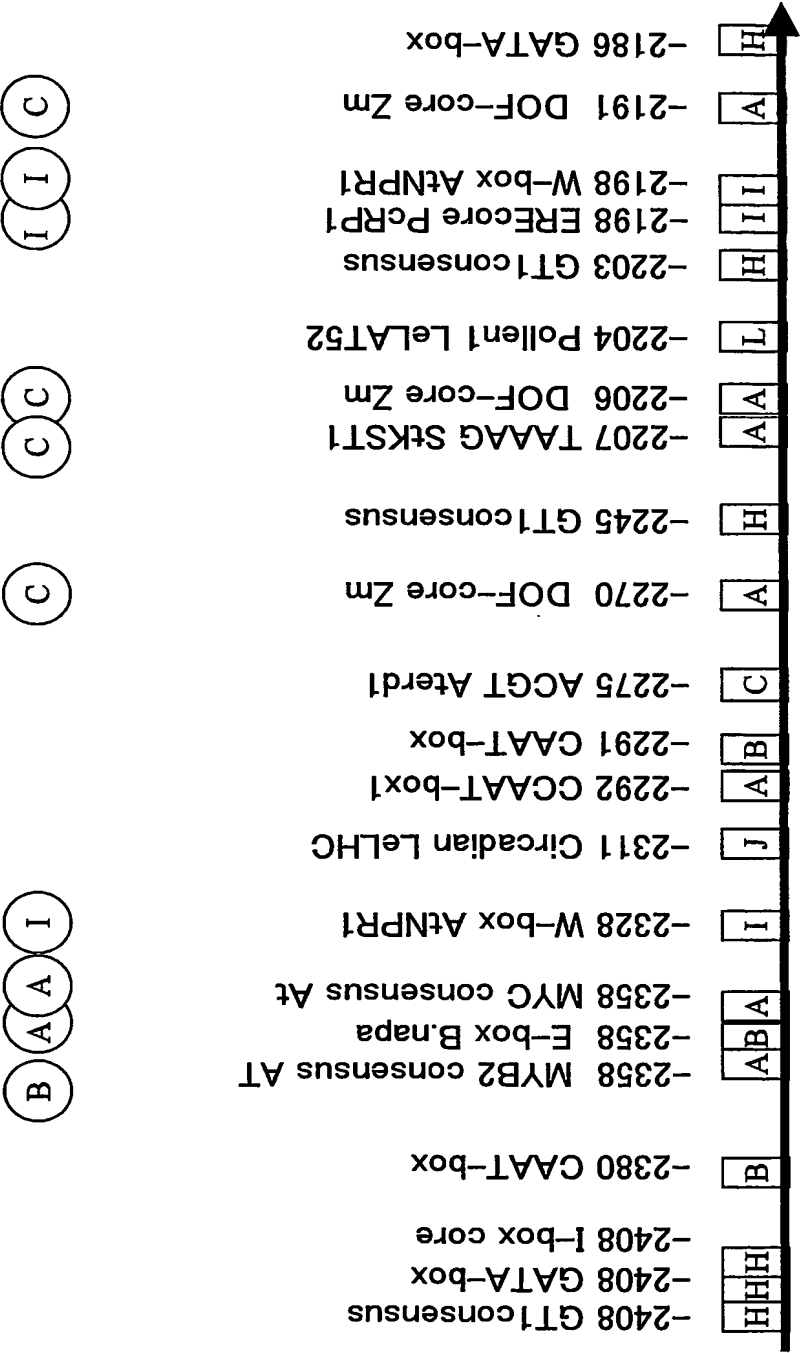
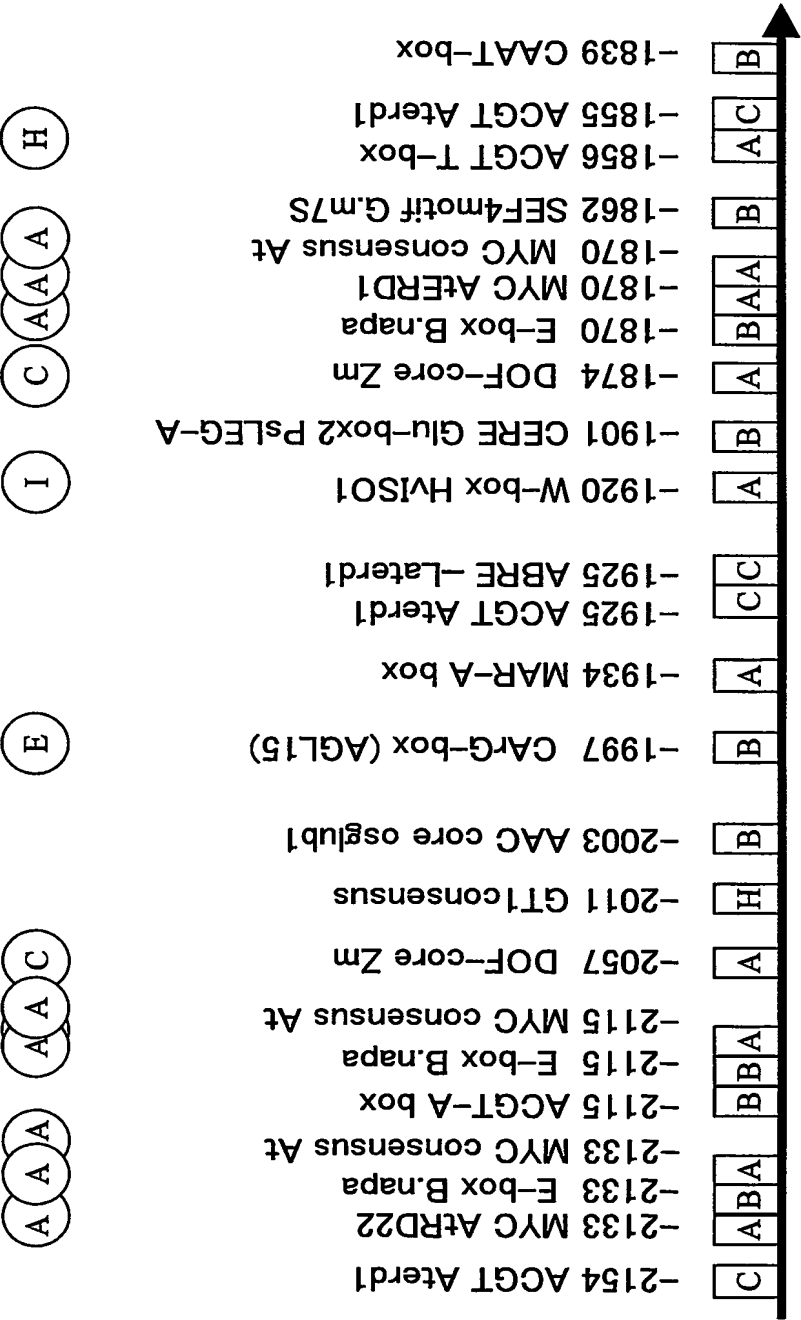


FIG. 11 (C)



9 2 / 1 2

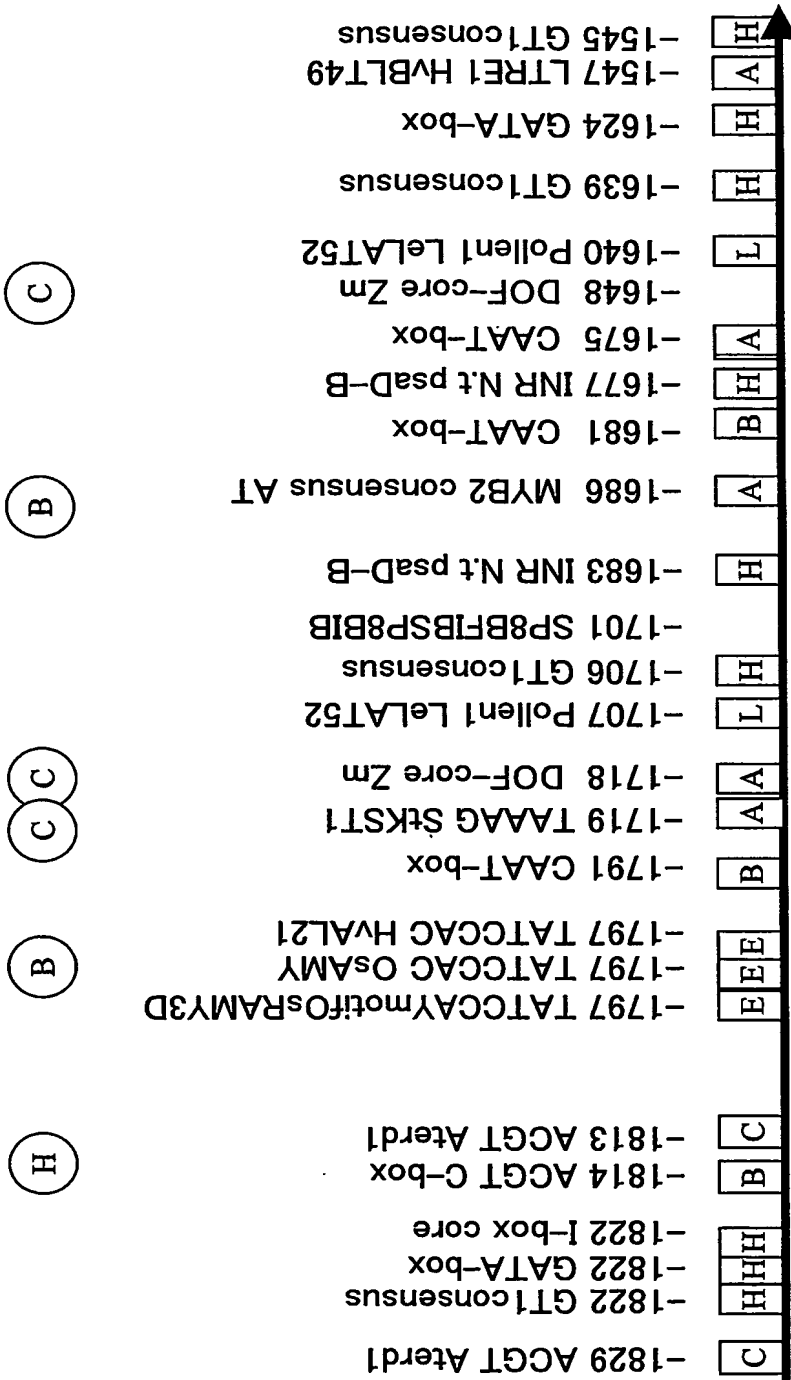
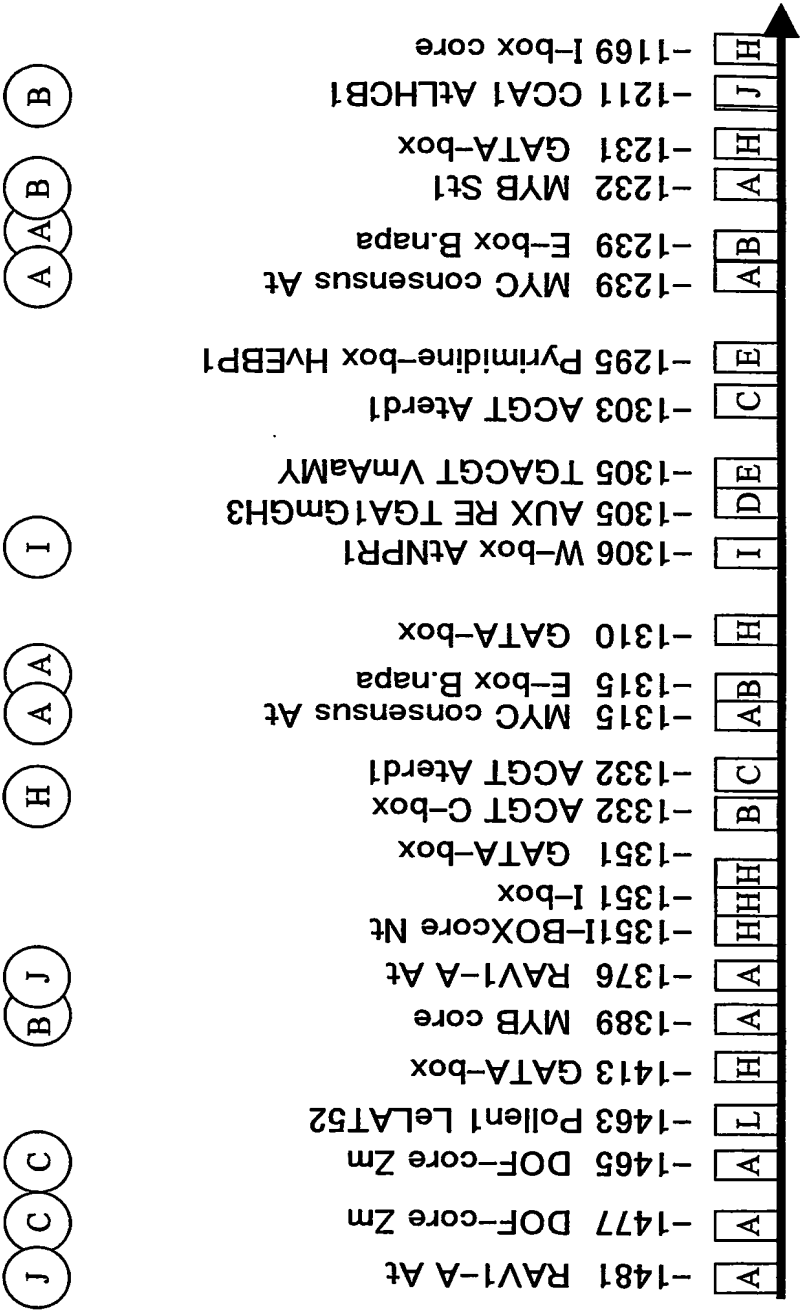


FIG. 11(D)

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FIG. 11 (E)



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FIG. 11 (F)

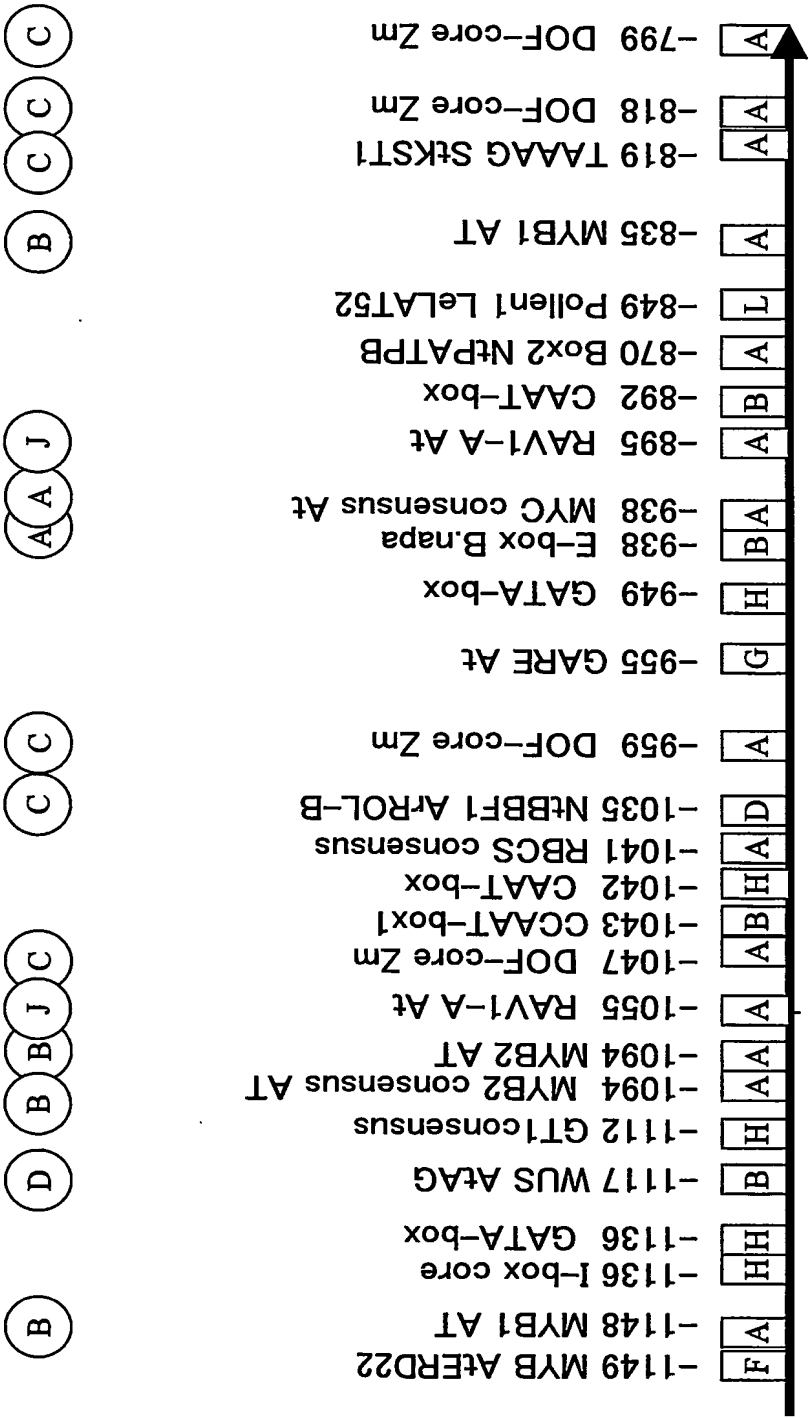
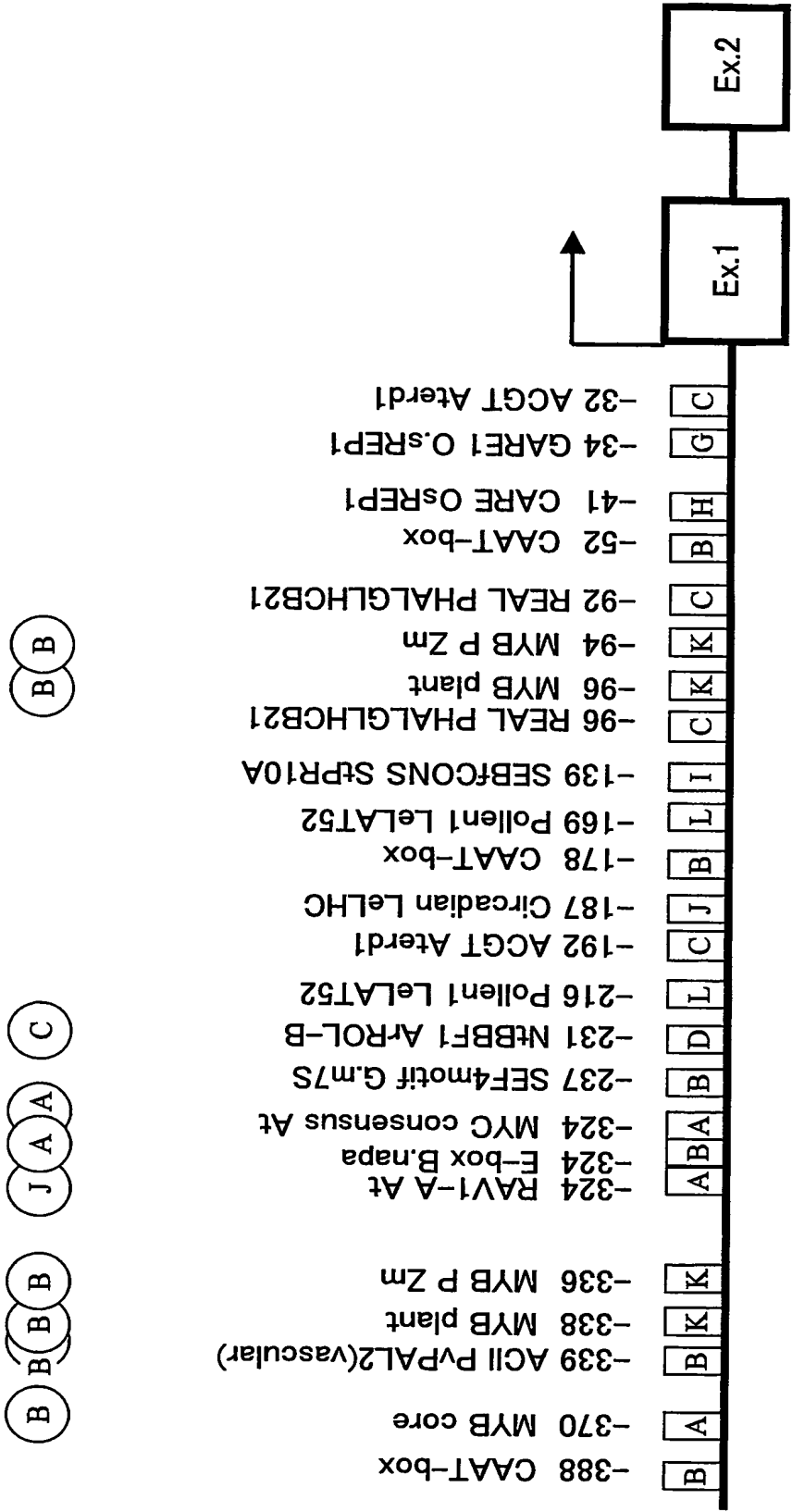


FIG. 11 (G)

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FIG. 11 (H)



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FIG. 12(a)

1st Intron of SST (S.indicum)

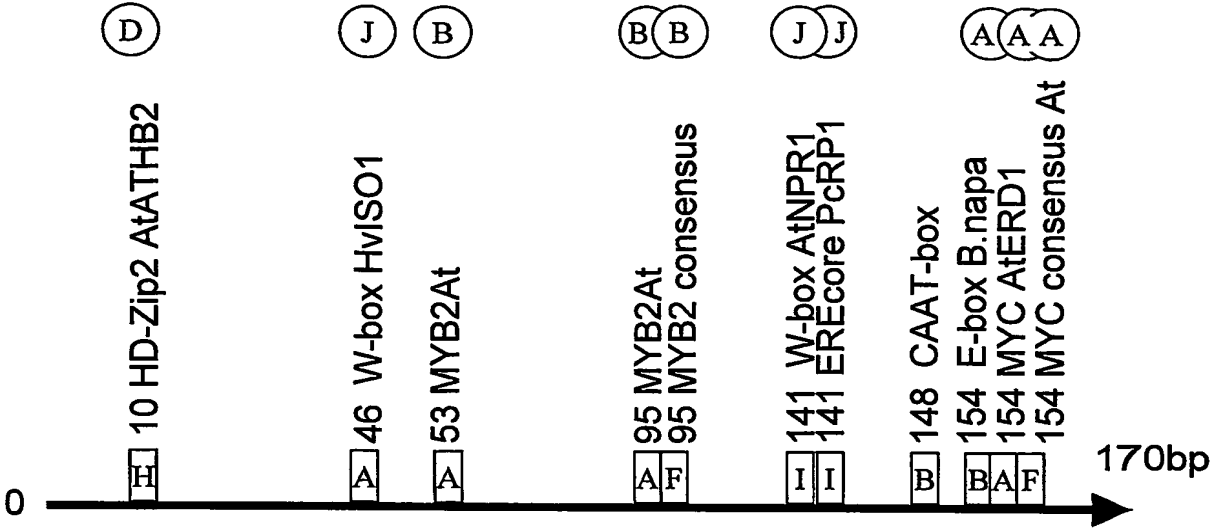


FIG. 12(b)

1st Intron of SrSST (S.radiatum)

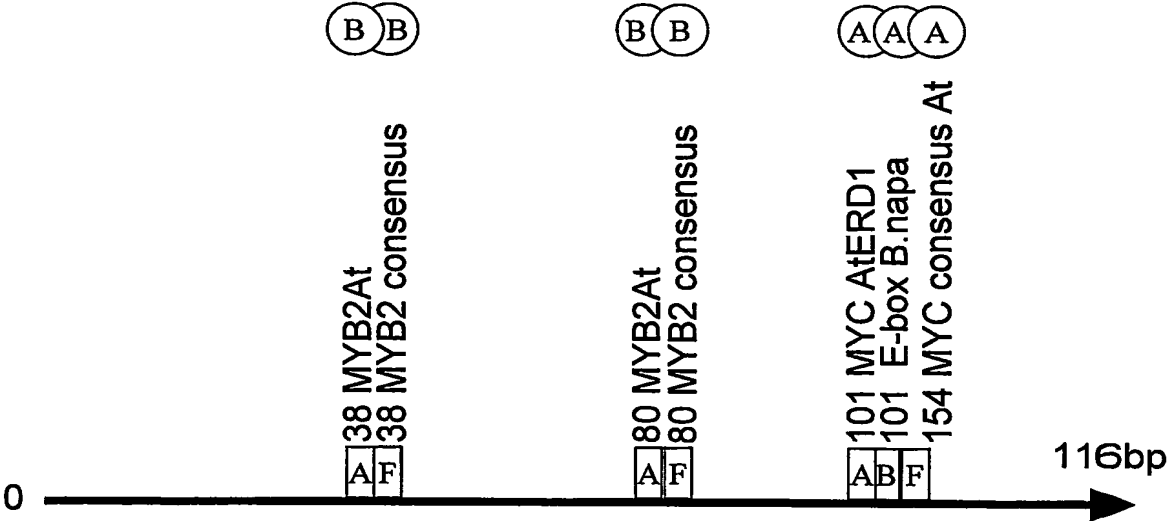


FIG. 12(c)

